

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/518,223A  
Source: 1Fw/b  
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IFW16

## RAW SEQUENCE LISTING

DATE: 09/01/2006

PATENT APPLICATION: US/10/518,223A

TIME: 10:48:14

Input Set : F:\00007135 030b-SEQ Listing from KMOB.TXT

Output Set: N:\CRF4\09012006\J518223A.raw

4 <110> APPLICANT: Cheng, Ning Man  
 5 Leung, Yun Chung  
 6 Lo, Wai Hung  
 8 <120> TITLE OF INVENTION: PHARMACEUTICAL PREPARATION AND METHOD OF  
 9 TREATMENT OF HUMAN MALIGNANCIES WITH ARGININE DEPRIVATION  
 12 <130> FILE REFERENCE: B001.001.NPRUS  
 14 <140> CURRENT APPLICATION NUMBER: 10/518,223A  
 15 <141> CURRENT FILING DATE: 2004-12-15  
 17 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/002665  
 18 <151> PRIOR FILING DATE: 2003-06-20  
 20 <150> PRIOR APPLICATION NUMBER: PCT/CN02/00635  
 21 <151> PRIOR FILING DATE: 2002-09-09  
 23 <150> PRIOR APPLICATION NUMBER: 60/390,757  
 24 <151> PRIOR FILING DATE: 2002-06-20  
 26 <160> NUMBER OF SEQ ID NOS: 9  
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 2002  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Homo sapiens  
 35 <400> SEQUENCE: 1  
 36 gaattgtacg tcaaagagat gaagcagaaa aacgtcgctg agaagaagct gaacgacaaa 60  
 37 aagtgaaatg cgagggaaatg ccaagaaaatg gtgattatga ggggtgtctat ttcaccaaaa 120  
 38 acggagaata tttattggaa ttaagagtct ctgggactgc tcttgtaaat gtccttgta 180  
 39 atttaaagga tattgacata acgaaatggt tgtgtaaaac agggagatata tattttgata 240  
 40 aggttaagaa atttgaataa gtactattc tttccatga cgtagaaaaat caaaagatta 300  
 41 taacagaatg ggagtcaactc cccagagagg cttaaccgaa acaatttgat tcataagaac 360  
 42 taatttagtag cgctttccaa tggaggcgct ttttatttg ggtagttgca taccactaaa 420  
 43 gatgttcagg tgcacatgag cattggagga aaggaacgct ttagggggaa gggaaacctt 480  
 44 taaacagtct taatccccct tgattttatg ttctctgtaa actgcgtccg gtaaatctca 540  
 45 ggatagacaa tcggcggtta acggctttag tgcggggca gtttagaaag aatatgattg 600  
 46 gagggattca tagatgcattt accatcacca tcatatgagc gccaagtcca gaaccatagg 660  
 47 gattatttggaa gtcctttct caaagggaca gccacagggaa ggggtggaaag aaggccctac 720  
 48 agtatttggaa aaggctggtc tgcttgagaa acttaaagaa caagagtgtg atgtgaagga 780  
 49 ttatgggac ctggccctttg ctgacatccc taatgacagt ccctttcaaa ttgtgaagaa 840  
 50 tccaaaggctt gttggaaaag caagcgagca gctggctggc aaggtggcac aagtcaagaa 900  
 51 gaacggaaaga atcagctgg tgcggggcg agaccacagt ttggcaatttga gaagcatctc 960  
 52 tggccatgcc agggtccacc ctgatcttgg agtcatctgg gtggatgctc acactgatat 1020  
 53 caacactcca ctgacaacca caagtggaaa cttgcatttgc caacctgtat ctggccctt 1080  
 54 gaagggaaaga aaaggaaaga ttcccgatgt gccaggattc tcctgggtga ctccctgtat 1140  
 55 atctgccaag gatattgtgt atattggctt gagagacgtg gaccctgggg aacactacat 1200  
 56 ttggaaaact ctaggcattt aatacttttcaatgactgaa gtggacagac taggaatttgg 1260  
 57 caaggtgatg gaagaaacac tcagctatct acttaggaaga aagaaaaggc caattcatct 1320

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58 aagtttgat gttgacggac tggacccatc tttcacacca gctactggca caccagtcgt 1380  
 59 gggaggtctg acatacagag aaggtctcta catcacagaa gaaatctaca aaacaggct 1440  
 60 actctcagga ttagatataa tgaagtgaa cccatccctg gggaaagacac cagaagaagt 1500  
 61 aactcgaaca gtgaacacag cagttgcaat aaccttggct ttttcggac ttgctcggga 1560  
 62 gggtaatcac aagcctattg actaccttaa cccacctaag taaatgtgga aacatccgt 1620  
 63 ataaatctca tagttaatgg cataattaga aagctaatca ttttcttaag catagagttt 1680  
 64 tccttctaaa gacttggct ttcagaaaaa ttttttcca attagtataa actctacaaa 1740  
 65 ttccctcttg gtgtaaaatt caagatgtgg aaattctaac tttttgaaa tttaaaaagct 1800  
 66 tatattttct aacttggcaa aagacttatac cttagaaaaga gaagtgtaca ttgatttcca 1860  
 67 attaaaaatt tgctggcatt aaaaataaagc acacttacat aagccccat acatagagtg 1920  
 68 ggactcttgg aatcaggaga caaagctacc acatgtgaa aggtactatg tgtccatgtc 1980  
 69 attcaaaaaa tgtgattcta ga 2002  
 71 <210> SEQ ID NO: 2  
 72 <211> LENGTH: 990  
 73 <212> TYPE: DNA  
 74 <213> ORGANISM: Artificial Sequence  
 76 <220> FEATURE:  
 77 <223> OTHER INFORMATION: Chimeric DNA sequence encoding human arginase I  
 78 and an N-terminal histidine tag  
 80 <400> SEQUENCE: 2  
 81 atg cat cac cat cac cat atg agc gcc aag tcc aga acc ata ggg 48  
 82 att att gga gct cct ttc tca aag gga cag cca cga gga ggg gtg gaa 96  
 83 gaa ggc cct aca gta ttg aga aag gct ggt ctg ctt gag aaa ctt aaa 144  
 84 gaa caa gag tgt gat gtg aag gat tat ggg gac ctg ccc ttt gct gac 192  
 85 atc cct aat gac agt ccc ttt caa att gtg aag aat cca agg tct gtg 240  
 86 gga aaa gca agc gag cag ctg gct ggc aag gtg gca caa gtc aag aag 288  
 87 aac gga aga atc agc ctg gtg ctg ggc gga gac cac agt ttg gca att 336  
 88 gga agc atc tct ggc cat gcc agg gtc cac cct gat ctt gga gtc atc 384  
 89 tgg gtg gat gct cac act gat atc aac act cca ctg aca acc aca agt 432  
 90 gga aac ttg cat gga caa cct gta tct ttc ctc ctg aag gaa cta aaa 480  
 91 gga aag att ccc gat gtg cca gga ttc tcc tgg gtg act ccc tgt ata 528  
 92 tct gcc aag gat att gtg tat att ggc ttg aga gac gtg gac cct ggg 576  
 93 gaa cac tac att ttg aaa act cta ggc att aaa tac ttt tca atg act 624  
 94 gaa gtg gac aga cta gga att ggc aag gtg atg gaa gaa aca ctc agc 672  
 95 tat cta cta gga aga aag aaa agg cca att cat cta agt ttt gat gtt 720  
 96 gac gga ctg gac cca tct ttc aca cca gct act ggc aca cca gtc gtg 768  
 97 gga ggt ctg aca tac aga gaa ggt ctc tac atc aca gaa gaa atc tac 816  
 98 aaa aca ggg cta ctc tca gga tta gat ata atg gaa gtg aac cca tcc 864  
 99 ctg ggg aag aca cca gaa gta act cga aca gtg aac aca gca gtt 912  
 100 gca ata acc ttg gct tgt ttc gga ctt gct cgg gag ggt aat cac aag 960  
 101 cct att gac tac ctt aac cca cct aag taa 990  
 103 <210> SEQ ID NO: 3  
 104 <211> LENGTH: 329  
 105 <212> TYPE: PRT  
 106 <213> ORGANISM: Artificial Sequence  
 108 <220> FEATURE:  
 109 <223> OTHER INFORMATION: Chimeric AA sequence of human arginase I and an  
 110 N-terminal histidine tag  
 112 <400> SEQUENCE: 3

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113 Met His His His His His Met Ser Ala Lys Ser Arg Thr Ile Gly  
 114 1 5 10 15  
 115 Ile Ile Gly Ala Pro Phe Ser Lys Gly Gln Pro Arg Gly Gly Val Glu  
 116 20 25 30  
 117 Glu Gly Pro Thr Val Leu Arg Lys Ala Gly Leu Leu Glu Lys Leu Lys  
 118 35 40 45  
 119 Glu Gln Glu Cys Asp Val Lys Asp Tyr Gly Asp Leu Pro Phe Ala Asp  
 120 50 55 60  
 121 Ile Pro Asn Asp Ser Pro Phe Gln Ile Val Lys Asn Pro Arg Ser Val  
 122 65 70 75 80  
 123 Gly Lys Ala Ser Glu Gln Leu Ala Gly Lys Val Ala Gln Val Lys Lys  
 124 85 90 95  
 125 Asn Gly Arg Ile Ser Leu Val Leu Gly Gly Asp His Ser Leu Ala Ile  
 126 100 105 110  
 127 Gly Ser Ile Ser Gly His Ala Arg Val His Pro Asp Leu Gly Val Ile  
 128 115 120 125  
 129 Trp Val Asp Ala His Thr Asp Ile Asn Thr Pro Leu Thr Thr Ser  
 130 130 135 140  
 131 Gly Asn Leu His Gly Gln Pro Val Ser Phe Leu Leu Lys Glu Leu Lys  
 132 145 150 155 160  
 133 Gly Lys Ile Pro Asp Val Pro Gly Phe Ser Trp Val Thr Pro Cys Ile  
 134 165 170 175  
 135 Ser Ala Lys Asp Ile Val Tyr Ile Gly Leu Arg Asp Val Asp Pro Gly  
 136 180 185 190  
 137 Glu His Tyr Ile Leu Lys Thr Leu Gly Ile Lys Tyr Phe Ser Met Thr  
 138 195 200 205  
 139 Glu Val Asp Arg Leu Gly Ile Gly Lys Val Met Glu Glu Thr Leu Ser  
 140 210 215 220  
 141 Tyr Leu Leu Gly Arg Lys Lys Arg Pro Ile His Leu Ser Phe Asp Val  
 142 225 230 235 240  
 143 Asp Gly Leu Asp Pro Ser Phe Thr Pro Ala Thr Gly Thr Pro Val Val  
 144 245 250 255  
 145 Gly Gly Leu Thr Tyr Arg Glu Gly Leu Tyr Ile Thr Glu Glu Ile Tyr  
 146 260 265 270  
 147 Lys Thr Gly Leu Leu Ser Gly Leu Asp Ile Met Glu Val Asn Pro Ser  
 148 275 280 285  
 149 Leu Gly Lys Thr Pro Glu Glu Val Thr Arg Thr Val Asn Thr Ala Val  
 150 290 295 300  
 151 Ala Ile Thr Leu Ala Cys Phe Gly Leu Ala Arg Glu Gly Asn His Lys  
 152 305 310 315 320  
 153 Pro Ile Asp Tyr Leu Asn Pro Pro Lys  
 154 325  
 157 <210> SEQ ID NO: 4  
 158 <211> LENGTH: 7  
 159 <212> TYPE: PRT  
 160 <213> ORGANISM: Artificial Sequence  
 162 <220> FEATURE:  
 163 <223> OTHER INFORMATION: 6x Histidine tag  
 165 <400> SEQUENCE: 4

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166 Met His His His His His  
 167 1 5  
 170 <210> SEQ ID NO: 5  
 171 <211> LENGTH: 33  
 172 <212> TYPE: DNA  
 173 <213> ORGANISM: Artificial Sequence  
 175 <220> FEATURE:  
 176 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence  
 178 <400> SEQUENCE: 5  
 179 ccaaaccata tgagcgccaa gtccagaacc ata 33  
 181 <210> SEQ ID NO: 6  
 182 <211> LENGTH: 39  
 183 <212> TYPE: DNA  
 184 <213> ORGANISM: Artificial Sequence  
 186 <220> FEATURE:  
 187 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence  
 189 <400> SEQUENCE: 6  
 190 ccaaactcta gaatcacatt ttttgaatga catggacac 39  
 192 <210> SEQ ID NO: 7  
 193 <211> LENGTH: 24  
 194 <212> TYPE: DNA  
 195 <213> ORGANISM: Artificial Sequence  
 197 <220> FEATURE:  
 198 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence  
 200 <400> SEQUENCE: 7  
 201 ctctggccat gccagggtcc accc 24  
 203 <210> SEQ ID NO: 8  
 204 <211> LENGTH: 969  
 205 <212> TYPE: DNA  
 206 <213> ORGANISM: Homo sapiens  
 208 <220> FEATURE:  
 209 <221> NAME/KEY: CDS  
 210 <222> LOCATION: (1)...(969)  
 212 <400> SEQUENCE: 8  
 213 atg agc gcc aag tcc aga acc ata ggg att att gga gct cct ttc tca 48  
 214 Met Ser Ala Lys Ser Arg Thr Ile Gly Ile Ile Gly Ala Pro Phe Ser  
 215 1 5 10 15  
 217 aag gga cag cca cga gga ggg gtg gaa gaa ggc cct aca gta ttg aga 96  
 218 Lys Gly Gln Pro Arg Gly Gly Val Glu Glu Gly Pro Thr Val Leu Arg  
 219 20 25 30  
 221 aag gct ggt ctg ctt gag aaa ctt aaa gaa caa gag tgt gat gtg aag 144  
 222 Lys Ala Gly Leu Leu Glu Lys Leu Lys Glu Gln Glu Cys Asp Val Lys  
 223 35 40 45  
 225 gat tat ggg gac ctg ccc ttt gct gac atc cct aat gac agt ccc ttt 192  
 226 Asp Tyr Gly Asp Leu Pro Phe Ala Asp Ile Pro Asn Asp Ser Pro Phe  
 227 50 55 60  
 229 caa att gtg aag aat cca agg tct gtg gga aaa gca agc gag cag ctg 240  
 230 Gln Ile Val Lys Asn Pro Arg Ser Val Gly Lys Ala Ser Glu Gln Leu  
 231 65 70 75 80

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233	gct	ggc	aag	gtg	gca	caa	gtc	aag	aac	gga	aga	atc	agc	ctg	gtg	288	
234	Ala	Gly	Lys	Val	Ala	Gln	Val	Lys	Lys	Asn	Gly	Arg	Ile	Ser	Leu	Val	
235																95	
237	ctg	ggc	gga	gac	cac	agt	ttg	gca	att	gga	agc	atc	tct	ggc	cat	gcc	336
238	Leu	Gly	Gly	Asp	His	Ser	Leu	Ala	Ile	Gly	Ser	Ile	Ser	Gly	His	Ala	
239																110	
241	agg	gtc	cac	cct	gat	ctt	gga	gtc	atc	tgg	gtg	gat	gct	cac	act	gat	384
242	Arg	Val	His	Pro	Asp	Leu	Gly	Val	Ile	Trp	Val	Asp	Ala	His	Thr	Asp	
243																125	
245	atc	aac	act	cca	ctg	aca	acc	aca	agt	gga	aac	ttg	cat	gga	caa	cct	432
246	Ile	Asn	Thr	Pro	Leu	Thr	Thr	Ser	Gly	Asn	Leu	His	Gly	Gln	Pro		
247																140	
249	gta	tct	ttc	ctc	ctg	aag	gaa	cta	aaa	gga	aag	att	ccc	gat	gtg	cca	480
250	Val	Ser	Phe	Leu	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Ile	Pro	Asp	Val	Pro	
251	145															160	
253	gga	ttc	tcc	tgg	gtg	act	ccc	tgt	ata	tct	gcc	aag	gat	att	gtg	tat	528
254	Gly	Phe	Ser	Trp	Val	Thr	Pro	Cys	Ile	Ser	Ala	Lys	Asp	Ile	Val	Tyr	
255																175	
257	att	ggc	ttg	aga	gac	gtg	gac	cct	ggg	gaa	cac	tac	att	ttg	aaa	act	576
258	Ile	Gly	Leu	Arg	Asp	Val	Asp	Pro	Gly	Glu	His	Tyr	Ile	Leu	Lys	Thr	
259																190	
261	cta	ggc	att	aaa	tac	ttt	tca	atg	act	gaa	gtg	gac	aga	cta	gga	att	624
262	Leu	Gly	Ile	Lys	Tyr	Phe	Ser	Met	Thr	Glu	Val	Asp	Arg	Leu	Gly	Ile	
263																205	
265	ggc	aag	gtg	atg	gaa	gaa	aca	ctc	agc	tat	cta	cta	gga	aga	aag	aaa	672
266	Gly	Lys	Val	Met	Glu	Glu	Thr	Leu	Ser	Tyr	Leu	Leu	Gly	Arg	Lys	Lys	
267																220	
269	agg	cca	att	cat	cta	agt	ttt	gat	gtt	gac	gga	ctg	gac	cca	tct	ttc	720
270	Arg	Pro	Ile	His	Leu	Ser	Phe	Asp	Val	Asp	Gly	Leu	Asp	Pro	Ser	Phe	
271	225															240	
273	aca	cca	gct	act	ggc	aca	cca	gtc	gtg	gga	ggt	ctg	aca	tac	aga	gaa	768
274	Thr	Pro	Ala	Thr	Gly	Thr	Pro	Val	Val	Gly	Gly	Leu	Thr	Tyr	Arg	Glu	
275																255	
277	ggt	ctc	tac	atc	aca	gaa	gaa	atc	tac	aaa	aca	ggg	cta	ctc	tca	gga	816
278	Gly	Leu	Tyr	Ile	Thr	Glu	Glu	Ile	Tyr	Lys	Thr	Gly	Leu	Leu	Ser	Gly	
279																270	
281	tta	gat	ata	atg	gaa	gtg	aac	cca	tcc	ctg	ggg	aag	aca	cca	gaa	gaa	864
282	Leu	Asp	Ile	Met	Glu	Val	Asn	Pro	Ser	Leu	Gly	Lys	Thr	Pro	Glu	Glu	
283																285	
285	gta	act	cga	aca	gtg	aac	aca	gca	gtt	gca	ata	acc	ttg	gct	tgt	ttc	912
286	Val	Thr	Arg	Thr	Val	Asn	Thr	Ala	Val	Ala	Ile	Thr	Leu	Ala	Cys	Phe	
287																300	
289	gga	ctt	gct	cg	gag	ggt	aat	cac	aag	cct	att	gac	tac	ctt	aac	cca	960
290	Gly	Leu	Ala	Arg	Glu	Gly	Asn	His	Lys	Pro	Ile	Asp	Tyr	Leu	Asn	Pro	
291	305															320	
293	cct	aag	taa													969	
294	Pro	Lys	*														
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299	<211>	LENGTH:	322														

**VERIFICATION SUMMARY**

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